

WEST Search History

DATE: Monday, December 29, 2003

Hide?	<u>Set</u> <u>Name</u>	<u>Query</u>	<u>Hit</u> <u>Count</u>
	<i>DB=USPT,PGPB,JPAB,EPAB,DWPI; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L8	L7 not L6	13
<input type="checkbox"/>	L7	L4 and marA.m/c. with (transcript\$ or activat\$5)	19
<input type="checkbox"/>	L6	L4 and reduc\$5 with (virulence or (marA with (transcript\$ or activat\$5)))	12
<input type="checkbox"/>	L5	L4 and reduce adj virulence	1
<input type="checkbox"/>	L4	(regulat\$5 or inhibit\$5 or reduc\$5 or modulat\$5) with (mar or marA)	5063
	<i>DB=PGPB,USPT,EPAB,JPAB,DWPI; PLUR=YES; OP=OR</i>		
<input type="checkbox"/>	L3	L2 and modulat\$	1
<input type="checkbox"/>	L2	(nfnB or nfnB or rdxA or nfsB) and (nitroreductase or NTR)	5
<input type="checkbox"/>	L1	(nfnB or nfsB or rdxA or (oxygen with insensitive or oxygen-insensitive) with nitoreductase) same (antibiotic or prodrug or antimicrob\$7 or anti-biot\$5 or anti-microbiot\$4 or virulence or infect\$8)	1

END OF SEARCH HISTORY



results of **BLAST**

BLASTP 2.2.6 [Apr-09-2003]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1072713772-6311-11077362477.BLASTQ4

Query=

(217 letters)

Database: All non-redundant GenBank CDS
translations+PDB+SwissProt+PIR+PRF

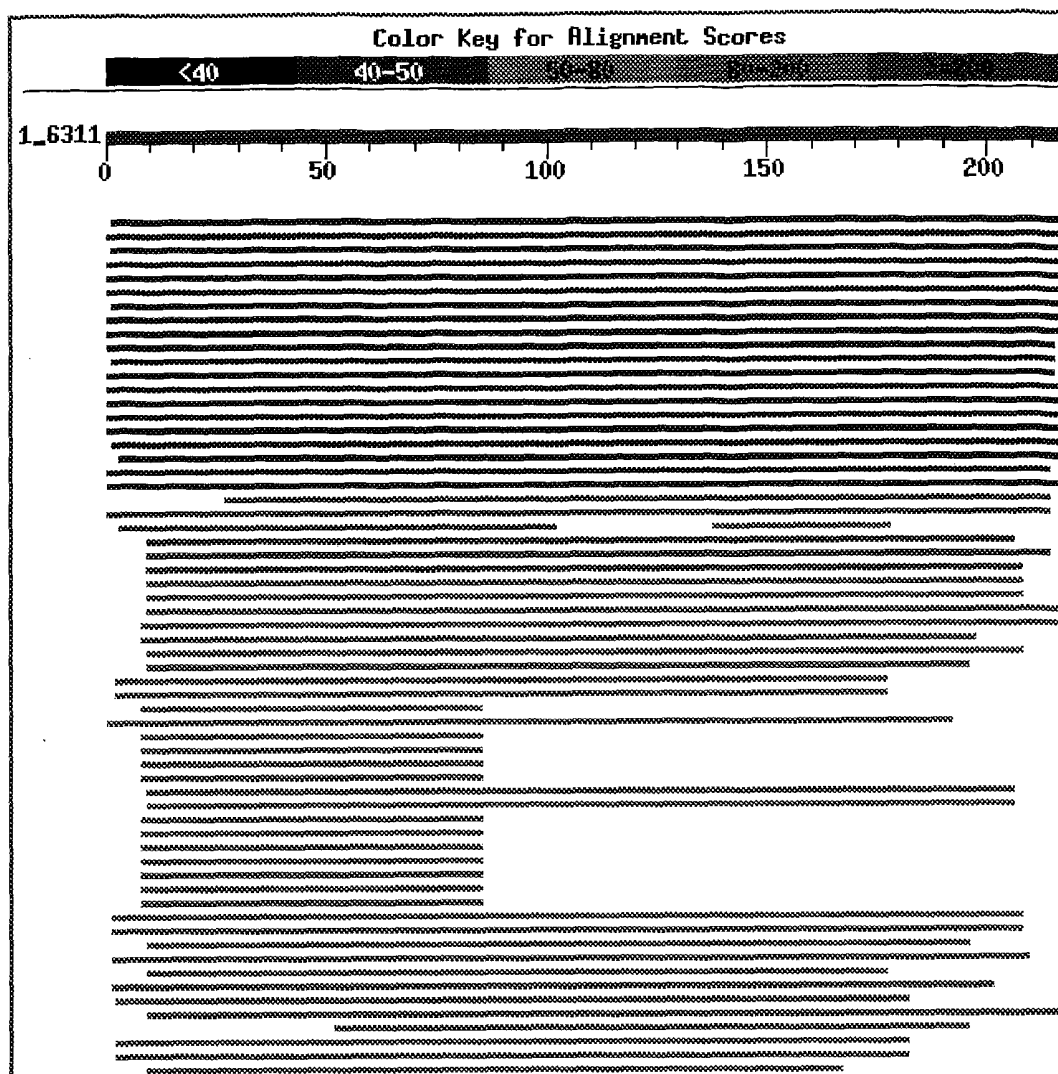
1,581,064 sequences; 518,058,112 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQ](#)

[Taxonomy reports](#)

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Related Structures

Sequences producing significant alignments:

Score E
(bits) Value

gi 15099965 gb AAK84182.1	glutathione-S-transferase-nitror...	412	e-114	
gi 16128561 ref NP_415110.1	oxygen-insensitive NAD(P)H nit...	399	e-110	
gi 9955254 pdb 1DS7 B	Chain B, A Minor Fmn-Dependent Nitror...	397	e-110	
gi 15800291 ref NP_286303.1	oxygen-insensitive NAD(P)H nit...	396	e-109	
gi 26246556 ref NP_752595.1	Oxygen-insensitive NAD(P)H nit...	391	e-108	
gi 30062032 ref NP_836203.1	oxygen-insensitive NAD(P)H nit...	389	e-107	
gi 14278494 pdb 1ICV A	Chain A, The Structure Of Escherichi...	386	e-106	
gi 16759538 ref NP_455155.1	oxygen-insensitive NAD(P)H nit...	356	1e-97	
gi 16763955 ref NP_459570.1	dihydropteridine reductase/oxy...	356	2e-97	
gi 400487 sp Q01234 NFNB_ENTCL	Oxygen-insensitive NAD(P)H n...	355	4e-97	
gi 7546304 pdb 1NEC A	Chain A, Nitroreductase From Enteroba...	352	2e-96	
gi 12232330 gb AAG48378.1	retro-nitroreductase [Enterobact...	352	4e-96	
gi 27367361 ref NP_762888.1	Nitroreductase [Vibrio vulnifi...	252	4e-66	
gi 28901446 ref NP_801101.1	oxygen-insensitive NAD(P)H nit...	246	3e-64	
gi 15601395 ref NP_233026.1	oxygen-insensitive NAD(P)H nit...	244	7e-64	

gi 34497699 ref NP_901914.1	oxygen-insensitive NAD(P)H nit...	238	4e-62
gi 24375212 ref NP_719255.1	oxygen-insensitive NAD(P)H nit...	218	7e-56
gi 23473136 ref ZP_00128432.1	COG0778: Nitroreductase [Des...	216	2e-55
gi 26989155 ref NP_744580.1	oxygen-insensitive NAD(P)H nit...	211	7e-54
gi 22984423 ref ZP_00029570.1	COG0778: Nitroreductase [Bur...	200	1e-50
gi 23104144 ref ZP_00090612.1	COG0778: Nitroreductase [Azo...	195	4e-49
gi 22980342 ref ZP_00026049.1	COG0778: Nitroreductase [Ral...	182	3e-45
gi 23476096 ref ZP_00131306.1	COG0778: Nitroreductase [Des...	108	7e-23
gi 6016045 sp P46072 FRA1 VIBFI	Major NAD(P)H-flavin oxidor...	99	4e-20
gi 28900963 ref NP_800618.1	putative NAD(P)H-flavin reduct...	94	2e-18
gi 22299744 ref NP_682991.1	nitroreductase [Thermosynechoc...	92	7e-18
gi 15890499 ref NP_356171.1	AGR_L_768p [Agrobacterium tume...	77	3e-13
gi 17938175 ref NP_534964.1	nitroreductase [Agrobacterium ...	75	8e-13
gi 16125698 ref NP_420262.1	nitroreductase family protein ...	74	2e-12
gi 32030652 ref ZP_00133458.1	COG0778: Nitroreductase [Hae...	69	8e-11
gi 23466765 ref ZP_00122352.1	COG0778: Nitroreductase [Hae...	69	8e-11
gi 32033912 ref ZP_00134183.1	COG0778: Nitroreductase [Act...	67	2e-10
gi 27468991 ref NP_765628.1	NAD(P)H-flavin oxidoreductase ...	64	2e-09
gi 15793971 ref NP_283793.1	putative NAD(P)H-flavin oxidor...	63	3e-09
gi 15676702 ref NP_273846.1	NAD(P)H nitroreductase, putati...	63	4e-09
gi 9858504 gb AAG01064.1	RdxA [Helicobacter pylori]	62	5e-09
gi 34558820 gb AAQ75164.1	NAD(P)H-flavin oxidoreductase [A...	62	7e-09
gi 9858534 gb AAG01077.1	RdxA [Helicobacter pylori]	62	7e-09
gi 17225177 gb AAL37285.1	oxygen-insensitive NADPH nitrore...	62	8e-09
gi 9858502 gb AAG01063.1	RdxA [Helicobacter pylori]	62	8e-09
gi 17225185 gb AAL37289.1	oxygen-insensitive NADPH nitrore...	62	9e-09
gi 23100581 ref NP_694048.1	NAD(P)H nitroreductase [Oceano...	62	9e-09
gi 16077850 ref NP_388664.1	similar to NAD(P)H-flavin oxid...	62	1e-08
gi 9858494 gb AAG01059.1	RdxA [Helicobacter pylori]	61	1e-08
gi 2564445 gb AAC46351.1	NADPH-linked flavin nitroreductas...	61	1e-08
gi 17225181 gb AAL37287.1	oxygen-insensitive NADPH nitrore...	61	1e-08
gi 9858514 gb AAG01069.1	RdxA [Helicobacter pylori] >gi 17...	61	1e-08
gi 9858492 gb AAG01058.1	RdxA [Helicobacter pylori]	61	1e-08
gi 19774226 gb AAL55409.1	NADPH nitroreductase RdxA [Helic...	61	1e-08
gi 9858531 gb AAG01076.1	RdxA [Helicobacter pylori]	61	1e-08
gi 18656027 emb CAC83804.1	RdxA protein [Helicobacter pylo...	61	1e-08
gi 18656017 emb CAC83799.1	RdxA protein [Helicobacter pylo...	61	2e-08
gi 262571 gb AAB24731.1	nitroreductase [Escherichia coli, ...	61	2e-08
gi 18656015 emb CAC83798.1	RdxA protein [Helicobacter pylori]	61	2e-08
gi 9858517 gb AAG01070.1	RdxA [Helicobacter pylori]	61	2e-08
gi 15611955 ref NP_223606.1	putative aldehyde dehydrogenas...	61	2e-08
gi 9858508 gb AAG01066.1	RdxA [Helicobacter pylori]	61	2e-08
gi 9858512 gb AAG01068.1	RdxA [Helicobacter pylori]	61	2e-08
gi 15645570 ref NP_207746.1	oxygen-insensitive NAD(P)H nit...	60	2e-08
gi 9858496 gb AAG01060.1	RdxA [Helicobacter pylori]	60	2e-08
gi 9858522 gb AAG01072.1	RdxA [Helicobacter pylori]	60	3e-08
gi 17225187 gb AAL37290.1	oxygen-insensitive NADPH nitrore...	59	5e-08
gi 17225183 gb AAL37288.1	truncated oxygen-insensitive NAD...	59	5e-08
gi 9858519 gb AAG01071.1	RdxA [Helicobacter pylori]	59	5e-08
gi 9858487 gb AAG01056.1	RdxA [Helicobacter pylori]	59	5e-08
gi 15612968 ref NP_241271.1	NAD(P)H-flavin oxidoreductase ...	59	6e-08
gi 16077633 ref NP_388447.1	similar to NADH dehydrogenase ...	59	8e-08
gi 9858510 gb AAG01067.1	RdxA [Helicobacter pylori]	59	8e-08
gi 21401255 ref NP_657240.1	Nitroreductase, Nitroreductase...	58	1e-07
gi 17225157 gb AAL37275.1	truncated oxygen-insensitive NAD...	58	1e-07
gi 9858528 gb AAG01075.1	RdxA [Helicobacter pylori]	58	1e-07
gi 9858506 gb AAG01065.1	RdxA [Helicobacter pylori]	58	1e-07
gi 13345216 gb AAK19260.1	RdxA [Helicobacter pylori]	58	1e-07
gi 15603697 ref NP_246771.1	unknown [Pasteurella multocida...	58	1e-07
gi 15925513 ref NP_373047.1	hypothetical protein [Staphylo...	57	2e-07

gi 17225173 gb AAL37283.1	oxygen-insensitive NADPH nitrore...	57	3e-07
gi 29346726 ref NP_810229.1	putative NADH dehydrogenase/NA...	56	5e-07
gi 28379407 ref NP_786299.1	nitroreductase [Lactobacillus ...	56	5e-07
gi 6018239 gb AAF01800.1	NADPH-flavin oxidoreductase [Heli...	55	7e-07
gi 15602598 ref NP_245670.1	unknown [Pasteurella multocida...	55	9e-07
gi 17225165 gb AAL37279.1	oxygen-insensitive NADPH nitrore...	55	1e-06
gi 9858526 gb AAG01074.1	RdxA [Helicobacter pylori]	54	3e-06
gi 18656019 emb CAC83800.1	RdxA protein [Helicobacter pylo...	54	3e-06
gi 9858524 gb AAG01073.1	RdxA [Helicobacter pylori]	53	3e-06
gi 17225189 gb AAL37291.1	oxygen-insensitive NADPH nitrore...	53	3e-06
gi 9858498 gb AAG01061.1	RdxA [Helicobacter pylori]	53	3e-06
gi 9858536 gb AAG01078.1	RdxA [Helicobacter pylori]	53	3e-06
gi 18656023 emb CAC83802.1	RdxA protein [Helicobacter pylo...	53	3e-06
gi 5924371 gb AAD56575.1	NADPH oxygen insensitive nitrored...	53	3e-06
gi 13537563 dbj BAB40800.1	NAD(P)H-flavin reductase [Shewa...	53	3e-06
gi 17225161 gb AAL37277.1	oxygen-insensitive NADPH nitrore...	53	3e-06
gi 13272370 gb AAK17124.1	RdxA [Helicobacter pylori]	53	3e-06
gi 9858500 gb AAG01062.1	RdxA [Helicobacter pylori]	53	4e-06
gi 6018241 gb AAF01801.1	NADPH-flavin oxidoreductase [Heli...	53	5e-06
gi 15611653 ref NP_223304.1	putative Oxidoreductase [Helic...	52	5e-06
gi 2564442 gb AAC46349.1	NADPH-linked flavin nitroreductas...	52	5e-06
gi 9858490 gb AAG01057.1	RdxA [Helicobacter pylori]	52	5e-06
gi 17225191 gb AAL37292.1	truncated oxygen-insensitive NAD...	52	5e-06
gi 33152545 ref NP_873898.1	NAD(P)H nitroreductase [Haemop...	52	5e-06
gi 16273193 ref NP_439431.1	NAD(P)H-flavin oxidoreductase ...	52	7e-06

Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|15099965|gb|AAK84182.1| glutathione-S-transferase-nitroreductase B fusion p
[synthetic construct]
Length = 442

Score = 412 bits (1058), Expect = e-114

Identities = 204/216 (94%), Positives = 204/216 (94%)

Query: 2 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA 61
DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA
Sbjct: 227 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA 286

Query: 62 KSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR 121
KSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR
Sbjct: 287 KSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR 346

Query: 122 KFFADMHRKDLHDDAEWMAKQVYLVNMGVFNXXXXXXXXXXXXXXXXXPIEGFDAAILDAEFGK 181
KFFADMHRKDLHDDAEWMAKQVYLVNMGVFN PIIEGFDAAILDAEFGK
Sbjct: 347 KFFADMHRKDLHDDAEWMAKQVYLVNMGVFNLLGVAALGLDAVPIIEGFDAAILDAEFGK 406

Query: 182 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV 217
GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV
Sbjct: 407 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV 442

☐ >gi|16128561|ref|NP_415110.1| oxygen-insensitive NAD(P)H nitroreductase [Escheri

gi|585554|sp|P38489|NFNB_ECOLI Oxygen-insensitive NAD(P)H nitroreductase (FMN-dep
nitroreductase) (Dihydropteridine reductase)

gi|2125984|pir||I67685 nitroreductase (EC 1.6.6.-) IB1 - Escherichia coli (strain

gi|9955253|pdb|1DS7|A Chain A, A Minor Fmn-Dependent Nitroreductase From Escher
B

gi|14278488|pdb|1ICR|A Chain A, The Structure Of Escherichia Coli Nitroreductas
With Nicotinic Acid

gi|14278489|pdb|1ICR|B Chain B, The Structure Of Escherichia Coli Nitroreductas
With Nicotinic Acid

gi|14278490|pdb|1ICU|A Chain A, The Structure Of Escherichia Coli Nitroreductas
With Nicotinic Acid

gi|14278491|pdb|1ICU|B Chain B, The Structure Of Escherichia Coli Nitroreductas
With Nicotinic Acid

gi|14278492|pdb|1ICU|C Chain C, The Structure Of Escherichia Coli Nitroreductas
With Nicotinic Acid

gi|14278493|pdb|1ICU|D Chain D, The Structure Of Escherichia Coli Nitroreductas
With Nicotinic Acid

gi|30749920|pdb|1005|A Chain A, Studies On The Nitroreductase Prodrug-Activatin
Crystal Structures Of The Enzyme Active Form And
Complexes With The Inhibitor Dicoumarol And
Dinitrobenzamide Prodrugs

gi|30749921|pdb|1005|B Chain B, Studies On The Nitroreductase Prodrug-Activatin
Crystal Structures Of The Enzyme Active Form And
Complexes With The Inhibitor Dicoumarol And
Dinitrobenzamide Prodrugs

gi|30749922|pdb|1006|A Chain A, Nitroreductase From E-Coli In Complex With The
Dinitrobenzamide Prodrug Sn23862

gi|30749923|pdb|1006|B Chain B, Nitroreductase From E-Coli In Complex With The
Dinitrobenzamide Prodrug Sn23862

gi|30749924|pdb|100N|A Chain A, Nitroreductase From E-Coli In Complex With The
Dinitrobenzamide Prodrug Sn27217

gi|30749925|pdb|100N|B Chain B, Nitroreductase From E-Coli In Complex With The
Dinitrobenzamide Prodrug Sn27217

gi|30749930|pdb|100Q|A Chain A, Nitroreductase From E-Coli In Complex With The
Dicoumarol

gi|30749931|pdb|100Q|B Chain B, Nitroreductase From E-Coli In Complex With The
Dicoumarol

gi|37926435|pdb|1IDT|A Chain A, Structural Studies On A Prodrug-Activating Syst
And Fmn-Dependent Nitroreductase

gi|37926436|pdb|1IDT|B Chain B, Structural Studies On A Prodrug-Activating Syst
And Fmn-Dependent Nitroreductase

gi|533421|gb|AAC43263.1| nitroreductase

gi|538227|dbj|BAA05004.1| oxygen-insensitive NAD(P)H nitroreductase [Escherichia

gi|1651240|dbj|BAA35218.1| Oxygen-insensitive NAD(P)H nitroreductase (EC 1.-.-.-)
[Escherichia coli K12]

gi|1778493|gb|AAB40776.1| oxygen-insensitive NAD(P)H nitroreductase [Escherichia

gi|1786792|gb|AAC73679.1| oxygen-insensitive NAD(P)H nitroreductase [Escherichia

Length = 217

Score = 399 bits (1026), Expect = e-110

Identities = 205/217 (94%), Positives = 205/217 (94%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV

Sbjct: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG



Sbjct: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNMGFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
RKFFADMHRKDLHDDAEWMAKQVYLVNMGF PIEGFDAAILDAEFGLKE

Sbjct: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNMGFLLGVAALGLDAVPIEGFDAAILDAEFGLKE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV

Sbjct: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217

 >gi|9955254|pdb|1DS7|B  Chain B, A Minor Fmn-Dependent Nitroreductase From Esci
B
Length = 217

Score = 397 bits (1020), Expect = e-110
Identities = 204/216 (94%), Positives = 204/216 (94%)

Query: 2 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA 61
DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA

Sbjct: 2 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA 61

Query: 62 KSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR 121
KSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR


Sbjct: 62 KSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR 121

Query: 122 KFFADMHRKDLHDDAEWMAKQVYLVNMGFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKEK 181
KFFADMHRKDLHDDAEWMAKQVYLVNMGF PIEGFDAAILDAEFGLKEK

Sbjct: 122 KFFADMHRKDLHDDAEWMAKQVYLVNMGFLLGVAALGLDAVPIEGFDAAILDAEFGLKEK 181

Query: 182 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV

Sbjct: 182 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217

 >gi|15800291|ref|NP_286303.1| oxygen-insensitive NAD(P)H nitroreductase [Escheri
EDL933]

gi|15829870|ref|NP_308643.1| oxygen-insensitive NAD(P)H nitroreductase [Escherich
O157:H7]

gi|25285227|pir||H90705 oxygen-insensitive NAD(P)H nitroreductase [imported] - Es
coli (strain O157:H7, substrain RIMD 0509952)

gi|25285228|pir||C85556 oxygen-insensitive NAD(P)H nitroreductase [imported] - Es
coli (strain O157:H7, substrain EDL933)

gi|12513463|gb|AAG54911.1| oxygen-insensitive NAD(P)H nitroreductase [Escherichia
EDL933]

gi|13360074|dbj|BAE34039.1| oxygen-insensitive NAD(P)H nitroreductase [Escherichi
O157:H7]

Length = 217

Score = 396 bits (1017), Expect = e-109
Identities = 203/217 (93%), Positives = 204/217 (94%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60

Sbjct: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
 Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
 AKSAAGNYVFNERK+LDASHVVVFCAKTAMDD WLKLVVDQEDADGRFATPEAKAANDKG
 Sbjct: 61 AKSAAGNYVFNERKILDASHVVVFCAKTAMDDAWLKLVVDQEDADGRFATPEAKAANDKG 120
 Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNGVNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
 RKFFADMHRKDLHDDAEWMAKQVYLVNGVNF PIEGFDAAILDAEFGLKE
 Sbjct: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNGVNFLLGVAALGLDAVPIEGFDAAILDAEFGLKE 180
 Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV
 Sbjct: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217

>gi|26246556|ref|NP_752595.1| Oxygen-insensitive NAD(P)H nitroreductase [Escheri
 gi|26106955|gb|AA079139.1| Oxygen-insensitive NAD(P)H nitroreductase [Escherichia
 Length = 217

Score = 391 bits (1005), Expect = e-108
 Identities = 202/217 (93%), Positives = 202/217 (93%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV
 Sbjct: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
 Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
 AKSAA NYVFNERKMLDASHVVVFCAKTAMDD WLKLVVDQEDADGRFATPEAKAANDKG
 Sbjct: 61 AKSAADNYVFNERKMLDASHVVVFCAKTAMDDAWLKLVVDQEDADGRFATPEAKAANDKG 120
 Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNGVNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
 RKFFADMHRKDLHDDAEWMAKQVYLVNGVNF PIEGFDAAILD EFGLKE
 Sbjct: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNGVNFLLGVAALGLDAVPIEGFDAAILDEEFGLKE 180
 Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV
 Sbjct: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217

>gi|30062032|ref|NP_836203.1| oxygen-insensitive NAD(P)H nitroreductase [Shigell
 str. 2457T]
 gi|30040276|gb|AAP16009.1| oxygen-insensitive NAD(P)H nitroreductase [Shigella fl
 str. 2457T]
 Length = 217

Score = 389 bits (1000), Expect = e-107
 Identities = 200/217 (92%), Positives = 202/217 (93%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV
 Sbjct: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
 Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
 AKSAAGNYVFNRK+LDASHVVVFCAKTAMDD WLKLVVDQEDADGRFATPEAKAANDKG
 Sbjct: 61 AKSAAGNYVFNRKILDASHVVVFCAKTAMDDAWLKLVVDQEDADGRFATPEAKAANDKG 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVGNFXXXXXXXXXXXXXPIEGFDAAILDAEFGGLKE 180
 RKFFA MHRKDLHDDAEWMAKQVYLVGNF PIEGFDAAILDAEFGGLKE
 Sbjct: 121 RKFFAYMHRKDLHDDAEWMAKQVYLVGNFLLGVAALGLDAVPIEGFDAAILDAEFGGLKE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV 217
 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQN TLTV
 Sbjct: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV 217

>gi|14278494|pdb|1ICV|A Chain A, The Structure Of Escherichia Coli Nitroreduct
 With Nicotinic Acid

gi|14278495|pdb|1ICV|B Chain B, The Structure Of Escherichia Coli Nitroreductas
 With Nicotinic Acid

gi|14278496|pdb|1ICV|C Chain C, The Structure Of Escherichia Coli Nitroreductas
 With Nicotinic Acid

gi|14278497|pdb|1ICV|D Chain D, The Structure Of Escherichia Coli Nitroreductas
 With Nicotinic Acid
 Length = 217

Score = 386 bits (992), Expect = e-106
 Identities = 200/216 (92%), Positives = 200/216 (92%)

Query: 2 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA 61
 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA
 Sbjct: 2 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA 61

Query: 62 KSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR 121
 KSAAGNYVFNERK LDASHVVVFCAKTA DDVWLKLVVDQEDADGRFATPEAKAANDKGR
 Sbjct: 62 KSAAGNYVFNERKXLDASHVVVFCAKTAXDDVWLKLVVDQEDADGRFATPEAKAANDKGR 121

Query: 122 KFFADMHRKDLHDDAEWMAKQVYLVGNFXXXXXXXXXXXXXPIEGFDAAILDAEFGGLKEK 181
 KFFAD HRKDLHDDAEW AKQVYLVGNF PIEGFDAAILDAEFGGLKEK
 Sbjct: 122 KFFADXHRKDLHDDAEWAKQVYLVGNFLLGVAALGLDAVPIEGFDAAILDAEFGGLKEK 181

Query: 182 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV 217
 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV
 Sbjct: 182 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV 217

>gi|16759538|ref|NP_455155.1| oxygen-insensitive NAD(P)H nitroreductase [Salmonella
 subsp. enterica serovar Typhi]

gi|29142689|ref|NP_806031.1| oxygen-insensitive NAD(P)H nitroreductase [Salmonella
 subsp. enterica serovar Typhi Ty2]

gi|25285229|pir|AD0573 oxygen-insensitive NAD(P)H nitroreductase [imported] - Sa
 enterica subsp. enterica serovar Typhi (strain CT18)

gi|16501830|emb|CAD05054.1| oxygen-insensitive NAD(P)H nitroreductase [Salmonella
 subsp. enterica serovar Typhi]

gi|29138320|gb|AA069891.1| oxygen-insensitive NAD(P)H nitroreductase [Salmonella
 subsp. enterica serovar Typhi Ty2]
 Length = 217

Score = 356 bits (914), Expect = 1e-97
 Identities = 180/217 (82%), Positives = 191/217 (88%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
 MDI+SVALKR+STKAFD SKKLT E+A+++KTLLQYSPSSTNSQPWHFIVASTEEGKARV

Sbjct: 1 MDIVSVALKRYSTKAFDPSKKLTAEADKVKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
AKSAAGNY FNERKMLDASHVVVFCAKTAMDD WL+ VVDQEDADGRFATPEAKAANDKG


Sbjct: 61 AKSAAGNYTFNERKMLDASHVVVFCAKTAMDDAWLQRVVDQEDADGRFATPEAKAANDKG 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNMGVNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
R+FFADMHR L DD +WMAKQVYLVNMGVNF PIEGFDA +LDAEFGLKE

Sbjct: 121 RRFFADMHRVSLKDDHQWMAKQVYLVNMGVNFLLGVAAMGLDAVPIEGFDAEVLDAEFGLKE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
KGYTSLVVVPVGHHS+EDFNA LPKSRLP TLTEV

Sbjct: 181 KGYTSLVVVPVGHHSIEDFNAGLPKSRLPLETTLTEV 217

 >gi|16763955|ref|NP_459570.1| dihydropteridine reductase/oxygen-insensitive NAD
nitroreductase [Salmonella typhimurium LT2]
gi|128354|sp|P15888|NFNB_SALTY Oxygen-insensitive NAD(P)H nitroreductase
gi|79103|pir||S08397 nitroreductase (EC 1.6.6.-) - Salmonella typhimurium
gi|47793|emb|CAA35113.1| unnamed protein product [Salmonella typhimurium]
gi|16419087|gb|AAL19529.1| dihydropteridine reductase [Salmonella typhimurium LT2]
Length = 217

Score = 356 bits (913), Expect = 2e-97
Identities = 181/217 (83%), Positives = 191/217 (88%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
MDI+SVAL+R+STKAFD SKKLT E+A++IKTLLQYSPSSTNSQPWHFIVASTEEGKARV

Sbjct: 1 MDIVSVALQRYSTKAFDPSKKLTAEADKIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
AKSAAGNY FNERKMLDASHVVVFCAKTAMDD WL+ VVDQEDADGRFATPEAKAANDKG







Sbjct: 61 AKSAAGNYTFNERKMLDASHVVVFCAKTAMDDAWLERVVDQEDADGRFATPEAKAANDKG 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNMGVNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
R+FFADMHR L DD +WMAKQVYLVNMGVNF PIEGFDA +LDAEFGLKE

Sbjct: 121 RRFFADMHRVSLKDDHQWMAKQVYLVNMGVNFLLGVAAMGLDAVPIEGFDAEVLDAEFGLKE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
KGYTSLVVVPVGHHSVEDFNA LPKSRLP TLTEV

Sbjct: 181 KGYTSLVVVPVGHHSVEDFNAGLPKSRLPLETTLTEV 217

 >gi|400487|sp|Q01234|NFNB_ENTCI Oxygen-insensitive NAD(P)H nitroreductase
gi|95566|pir||A38686 nitroreductase (EC 1.6.6.-) - Enterobacter cloacae
gi|20150964|pdb|1KQB|A  Chain A, Structure Of Nitroreductase From E. Cloacae Com
Inhibitor Benzoate
gi|20150965|pdb|1KQB|B  Chain B, Structure Of Nitroreductase From E. Cloacae Com
Inhibitor Benzoate
gi|20150966|pdb|1KQB|C  Chain C, Structure Of Nitroreductase From E. Cloacae Com
Inhibitor Benzoate
gi|20150967|pdb|1KQB|D  Chain D, Structure Of Nitroreductase From E. Cloacae Com
Inhibitor Benzoate
gi|20150968|pdb|1KQC|A  Chain A, Structure Of Nitroreductase From E. Cloacae Com
Inhibitor Acetate

gi|20150969|pdb|1KQC|B Chain B, Structure Of Nitroreductase From E. Cloacae Com Inhibitor Acetate

gi|20150970|pdb|1KQC|C Chain C, Structure Of Nitroreductase From E. Cloacae Com Inhibitor Acetate

gi|20150971|pdb|1KQC|D Chain D, Structure Of Nitroreductase From E. Cloacae Com Inhibitor Acetate

gi|20150972|pdb|1KQD|A Chain A, Structure Of Nitroreductase From E. Cloacae Bou Reduced Flavin Mononucleotide (Fmn)

gi|20150973|pdb|1KQD|B Chain B, Structure Of Nitroreductase From E. Cloacae Bou Reduced Flavin Mononucleotide (Fmn)

gi|20150974|pdb|1KQD|C Chain C, Structure Of Nitroreductase From E. Cloacae Bou Reduced Flavin Mononucleotide (Fmn)

gi|20150975|pdb|1KQD|D Chain D, Structure Of Nitroreductase From E. Cloacae Bou Reduced Flavin Mononucleotide (Fmn)

gi|148362|gb|AAA62801.1| oxygen-insensitive NAD(P)H nitroreductase
Length = 217

Score = 355 bits (910), Expect = 4e-97
Identities = 181/216 (83%), Positives = 190/216 (87%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEELGKARV 60
MDIISVALKRHSTKAFDASKKLT E+AE+IKTLLQYSPSSTNSQPWHFIVASTEELGKARV

Sbjct: 1 MDIISVALKRHSTKAFDASKKLTAEAEAEIKTLLQYSPSSTNSQPWHFIVASTEELGKARV 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
AKSAAG YVFNERKMLDASHVVVFCAKTAMDD WL+ VVDQE+ADGRF TPEAKAAN KG

Sbjct: 61 AKSAAGTYVFNERKMLDASHVVVFCAKTAMDDAWLERVVDQEEADGRFNTPEAKAANHKG 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLNVGNFXXXXXXXXXXXXXPIEGFDAAILDAEFGGLKE 180
R +FADMHR DL DD +WMAKQVYLNVGNF PIEGFDAAILD EFGGLKE

Sbjct: 121 RTYFADMHRVDLKDQDQWMAKQVYLNVGNFLLGVGAMGLDAVPIEGFDAAILDEEFGGLKE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTE 216
KG+TSLVVVPVGHHSVEDFNATLPKSRLP + +TE

Sbjct: 181 KGFTSLVVVPVGHHSVEDFNATLPKSRLPLSTIVTE 216

>gi|7546304|pdb|1NEC|A Chain A, Nitroreductase From Enterobacter Cloacae

gi|7546305|pdb|1NEC|B Chain B, Nitroreductase From Enterobacter Cloacae

gi|7546306|pdb|1NEC|C Chain C, Nitroreductase From Enterobacter Cloacae

gi|7546307|pdb|1NEC|D Chain D, Nitroreductase From Enterobacter Cloacae
Length = 216

Score = 352 bits (904), Expect = 2e-96
Identities = 180/215 (83%), Positives = 189/215 (87%)

Query: 2 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEELGKARVA 61
DIISVALKRHSTKAFDASKKLT E+AE+IKTLLQYSPSSTNSQPWHFIVASTEELGKARVA

Sbjct: 1 DIISVALKRHSTKAFDASKKLTAEAEAEIKTLLQYSPSSTNSQPWHFIVASTEELGKARVA 60

Query: 62 KSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR 121
KSAAG YVFNERKMLDASHVVVFCAKTAMDD WL+ VVDQE+ADGRF TPEAKAAN KGR

Sbjct: 61 KSAAGTYVFNERKMLDASHVVVFCAKTAMDDAWLERVVDQEEADGRFNTPEAKAANHKG 120

Query: 122 KFFADMHRKDLHDDAEWMAKQVYLNVGNFXXXXXXXXXXXXXPIEGFDAAILDAEFGGLKE 181

+FADMHR DL DD +WMAKQVYLVNGNF PIEGFDAAILD EFGLKEK
 Sbjct: 121 TYFADMHRVDLKDDQWMAKQVYLVNGNELLGVGAMGLDAVPIEGFDAAILDEEFGLKEK 180

Query: 182 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTE 216
 G+TSLVVVPVGHHSVEDFNATLPKSRLP + +TE
 Sbjct: 181 GFTSLVVVPVGHHSVEDFNATLPKSRLPLSTIVTE 215

☐ >gi|12232330|gb|AAG48378.1| retro-nitroreductase [Enterobacter cloacae]
 Length = 217

Score = 352 bits (902), Expect = 4e-96
 Identities = 178/216 (82%), Positives = 189/216 (87%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEELKARV 60
 MDIISVALKRHSTKAFD SKKLT E+AE+IKTLLQYSPSSTNSQPWHFI+ASTEELKARV
 Sbjct: 1 MDIISVALKRHSTKAFDPSKKLTAEAEKIKTLLQYSPSSTNSQPWHFI+ASTEELKARV 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
 AKSAAG YVNERKM+DASHVVVFCAKTAMDD WL+ VVDQE+ADGRF TPEAKAAN KG
 Sbjct: 61 AKSAAGTYVFNERKMDASHVVVFCAKTAMDDAWLERVVDQEEADGRFNTPEAKAANHKG 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNGNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
 R +FADMHR DL DD +WMAKQVYLVNGNF PIEGFDAAILD EFGLKE
 Sbjct: 121 RCFADMHRVDLKDDQWMAKQVYLVNGNELLGVAALGLDAVPIEGFDAAILDDEFGLKE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTE 216
 KG+TSLVVVPVGHHSVEDFNATLPKSRLP + +TE
 Sbjct: 181 KGFTSLVVVPVGHHSVEDFNATLPKSRLPLSTIVTE 216

☐ >gi|27367361|ref|NP_762888.1| Nitroreductase [Vibrio vulnificus CMCP6]
 gi|37677115|ref|NP_937511.1| nitroreductase [Vibrio vulnificus YJ016]
 gi|27358930|gb|AAO07878.1| Nitroreductase [Vibrio vulnificus CMCP6]
 gi|37201660|dbj|BAC97481.1| nitroreductase [Vibrio vulnificus YJ016]
 Length = 217

Score = 252 bits (643), Expect = 4e-66
 Identities = 126/217 (58%), Positives = 154/217 (70%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEELKARV 60
 M I+ A R+STKAFDAS+KL E+ +K L++ S SS NSQPWHFIVAS+EEGKAR+
 Sbjct: 1 MTIVQAAQSRYSTKAFDASRKLPEEKVAAVKELIRMSASSVNSQPWHFIVASSEEGKARI 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
 AK+ G + FNERK+LDASHVVVFCAKTA+D+ +L +++ ED DGRFA EAK G
 Sbjct: 61 AKATQGGFAFNERKILDASHVVVFCAKTAIDEAYLLDLLESEDKGRFADVEAKNGMHAG 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNGNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
 R FF +MHR DL D WM KQVYLVNG PIEGFDA +LD EFGL+E
 Sbjct: 121 RSFFVNMHRFDLKDAAHWMKQVYLVNGTLLLGASAMEIDAVPIEGFDAKVLDEEFGLRE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
 KG+TS+V+VP+G+HS +DFNA LPKSR TE+
 Sbjct: 181 KGFTSVVIVPLGYHSEDDFNALPKSRWSAETVFTEI 217

☐ >[gi|28901446|ref|NP_801101.1|](#) oxygen-insensitive NAD(P)H nitroreductase [Vibrio RIMD 2210633]
[gi|28809993|dbj|BAC62934.1|](#) oxygen-insensitive NAD(P)H nitroreductase [Vibrio par Length = 217

Score = 246 bits (627), Expect = 3e-64
 Identities = 119/217 (54%), Positives = 154/217 (70%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEELGKARV 60
 MDI+ A R+STK FD ++KL E+ + +K L+++SPSS NSQPWHFI+ASTEELGK R+
 Sbjct: 1 MDIVQAAKSRYSTKVFDPTKLPQEKIDAVKELIRFSPSSVNSQPWHFILASTEELGKQRI 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
 AK+A NY FN K+L+ASHV+VFCAKT +D+ +++ ++ QE+ DGRF T EAKAA G
 Sbjct: 61 AKAAQENYAFNAKILNASHVLVFCAMTGIDNDYIEALMAQEEKDGRFPTEEAKAAVRGG 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNNGFXXXXXXXXXXXXXPIEGFDAAILDAEFLKE 180
 R +F +MHR DL D WM KQVYLVNG PIEGFD +LD EFGL+E
 Sbjct: 121 RSYFVNLMHRFDLKDANHWMEKQVYLVNGTLLLGASTLEIDAVPIEGFDPKVLDEEFGLRE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
 KGYTS+V+VP+G+H+ +DFNA PKSR TE+
 Sbjct: 181 KGYTSVVIVPLGYHAEDDFNAKTPKSRWDAETVFTEI 217

☐ >[gi|15601395|ref|NP_233026.1|](#) oxygen-insensitive NAD(P)H nitroreductase [Vibrio biovar eltor str. N16961]
[gi|11355761|pir|C82436](#) oxygen-insensitive NAD(P)H nitroreductase VCA0637 [import Vibrio cholerae (strain N16961 serogroup O1)
[gi|9658051|gb|AAF96538.1|](#) oxygen-insensitive NAD(P)H nitroreductase [Vibrio cholerae biovar eltor str. N16961]
 Length = 217

Score = 244 bits (623), Expect = 7e-64
 Identities = 116/217 (53%), Positives = 153/217 (70%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEELGKARV 60
 M+I+ + R+STKAFDAS+KL+ +Q +K L++ S SS NSQPWHFI+A ++EGK R+
 Sbjct: 1 MNIVQASQSRYSTKAFDASRKLSQQVADLKLVRMSASSVNSQPWHFILAGSDEGKTRI 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
 AK+ G + FNERK+LDASHV+VFCAKT++DD +L ++D ED DGRFA EAK
 Sbjct: 61 AKATQGGFSFNERKILDASHVMVFCAMTSIDDAYLLSLLDNEDKDGRFANEEAKTGMHGA 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNNGFXXXXXXXXXXXXXPIEGFDAAILDAEFLKE 180
 R +F ++HR++L+D WM KQVYLVNG PIEGFDA +L+ EFGL E
 Sbjct: 121 RSYFVNLMHRENLDNAEHWMQKQVYLVNGTLLLGAAAMGIDAVPIEGFDAQVLNEEFGLTE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
 KG+ S+V+VP+G HS +DFNA LPKSR P TE+
 Sbjct: 181 KGFNSVVIVPLGFHSEDDFNALPKSRWPAAVFTTEL 217

☐ >[gi|34497699|ref|NP_901914.1|](#) oxygen-insensitive NAD(P)H nitroreductase [Chromobacterium violaceum ATCC 12472]
[gi|34103555|gb|AAQ59916.1|](#) oxygen-insensitive NAD(P)H nitroreductase [Chromobacterium violaceum ATCC 12472]

violaceum ATCC 12472]
Length = 217

Score = 238 bits (608), Expect = 4e-62
Identities = 117/217 (53%), Positives = 148/217 (68%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
M+I A R++TKAFD +L+ Q EQI+TLL++SPSSTNSQPWHF +A ++E KARV
Sbjct: 1 MNIAHYAQTRYTTKAFDPGFRLSAGQIEQIETLLRHSPSSTNSQPWHFFIAGSDESKARV 60

Query: 61 AKSAAGNYVFNERNKMLDASHVVVFCAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
AK+ A Y FN+ K+L+ASHVVVFC + A+DD +L+ ++DQE+ DGRFA+PEA+A KG
Sbjct: 61 AKATADGYAFNQAKVLNASHVVVFCRAALDDAYLRTLDDQEEERDGRFASPEARAGQHK 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVGNFXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
R FADMHR +L D WM KQVYL VG PIEGFD L E GL+E
Sbjct: 121 RSHFADMHRFELRDAPHWMEKQVYLAAGTLLLGAAALEIDACPIEGFDQRTLGEELGLRE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
KG + V+V +G S EDFNA LPKSRLP +T +
Sbjct: 181 KGLIASVIVALGRRSDEDFNARLPKSRLPAEAVITRL 217

☐ >[gi|24375212|ref|NP_719255.1|](#) oxygen-insensitive NAD(P)H nitroreductase [Shewanella MR-1]
[gi|24350000|gb|AA056699.1|](#) oxygen-insensitive NAD(P)H nitroreductase [Shewanella MR-1]
Length = 217

Score = 218 bits (555), Expect = 7e-56
Identities = 112/216 (51%), Positives = 144/216 (66%), Gaps = 1/216 (0%)

Query: 2 DIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVA 61
D+ +A KR++TKAFD +K + ++ IKTLLQ+SPSSTNSQPWHF++A T EGKA +A
Sbjct: 3 DLSFLAKKRYTTKAFDPTKIIPDKIADIKTLLQFSPSSTNSQPWHFVLAGTAEGKALIA 62

Query: 62 KSAAGNYVFNERNKMLDASHVVVFCAMDDVWLKLVVDQEDADGRFATPEAKAANDKGR 121
+ A +Y FN +K+LDASHVVV C +T +D+ L V++QE DGRFA EAK GR
Sbjct: 63 Q-ATEHYAFNTQKILDASHVVVLCRTTQLDEAHLQVLEQEAKDGRFANEEAKQGQHNGR 121

Query: 122 KFFADMHRKDLHDDAEWMAKQVYLVGNFXXXXXXXXXXXXPIEGFDAAILDAEFGLKEK 181
FFA+MH+ +L D WM KQVYL +G PIEGFD L+ GL+EK
Sbjct: 122 SFFANMHKFKELKDAQHWMEKQVYLAAGTLLMLGASVLDIDACPIEGFDATKLNQVLGLREK 181

Query: 182 GYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
G + VVV +G+ S EDFNA LPKSRL Q + TE+
Sbjct: 182 GLCASVVVALGYRSEEDFNAKLPSRLAQEVIFTEI 217

☐ >[gi|23473136|ref|ZP_00128432.1|](#) COG0778: Nitroreductase [Desulfovibrio desulfur] Length = 238

Score = 216 bits (551), Expect = 2e-55
Identities = 104/214 (48%), Positives = 138/214 (64%)

Query: 4 ISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKS 63
I R++TK FD ++L E + +K +LQ SPSSTNSQPWHF++A T+EG+ RVAK+

Sbjct: 25 IEALTTRYTTKKFDPDRRLDAETVQAVKDILQLSPSSTNSQPWHFVIAGTDEGRQVAKA 84

Query: 64 AAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKF 123
A G Y FN K+ DASHVVV C KT +D + V++QE+ DGRF + E KAA N KGR+F


Sbjct: 85 AHGVYAFNASKICDASHVVVLCTKTDIDTEYTTQVLEQEEQDGRFPSEETKAANRKGREF 144

Query: 124 FADMHRKDLHDDAEWMAKQVYLVNGFNXXXXXXXXXXXXPIEGFDAAILDAEFGLKEKGY 183
FA +HR +L D WM KQ ++ +GN P+EGFD +L+ E GL EKG Y

Sbjct: 145 FAMLHRNELQDAFWHMEKQTFIALGNLLSGAAHLGIHACPMEGFDHEVLEKELGLTEKGY 204

Query: 184 TSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV 217
V+V +G + +DFNA PKSR PQ +TE+

Sbjct: 205 KPSVIVALGFSAADDFNAVTPKSRWPQERIITEI 238

 >gi|26989155|ref|NP_744580.1| oxygen-insensitive NAD(P)H nitroreductase [Pseudor
KT2440]

gi|22347819|gb|AAM95987.1| oxygen-insensitive NADPH nitroreductase [Pseudomonas p
gi|24983992|gb|AAN68044.1| oxygen-insensitive NAD(P)H nitroreductase [Pseudomonas
KT2440]

Length = 217

Score = 211 bits (537), Expect = 7e-54
Identities = 103/215 (47%), Positives = 144/215 (66%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
MD +S+A +R++TKA+DAS+++ + + L++SPSS NSQPWHFIVA T EGKA +

Sbjct: 1 MDTVSLAKRRYTTKAYDASRRIPQATVDALLEQLRHSPSSVNSQPWHFIVADTAEGKALL 60

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
AKS A Y +N +K+LDASHV+VFC +T M + L V+DQE ADGRF +A+A ++


Sbjct: 61 AKSTAEGYAYNTQKLLDASHVIVFCTRTEMTEEHLNAVLDQEAADGRFRDEQARAGQNQS 120

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNGFNXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180
R+ + ++HR D D WM KQ YL +G PIEGFD+ +LDAE GL+E

Sbjct: 121 RRHYVNLHRFDQKDVQHWMEKQTYLALGTALLGAAAHGLDATPIEGFDSKVLD AELGLRE 180

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLT 215
+G+TS+V++ +G+ S DFNA L KSRLP + T

Sbjct: 181 RGFTSVVILSLGYRSEADFNAGLNKSRLPASQVFT 215

 >gi|22984423|ref|ZP_00029570.1| COG0778: Nitroreductase [Burkholderia fungorum]
Length = 233

Score = 200 bits (509), Expect = 1e-50
Identities = 100/217 (46%), Positives = 142/217 (65%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARV 60
++I A KR+STKAFD ++K+ E Q++ L+++SPSS NSQPWHF+VAS+++ KARV

Sbjct: 17 VNIAGYAKKRYSTKAFDPARKVPDETIAQLRELIRFSPSSVNSQPWHFVVASDDAKARV 76

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
AK+A G + +NE K+ +ASHV V CA+ +DDV L V+ QE+ DGRF + +A+ A

Sbjct: 77 AKAAQGRFAYNEPKVRNASHVFVLCARVLIDDVHLASVLLQEENDGRFVSADARNAQRNS 136

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVNGFNXXXXXXXXXXXXPIEGFDAAILDAEFGLKE 180

R+ + D HR +L D WM KQVYL +G P+EGFDA +LD E GL+
 Sbjct: 137 RQGYVDTHRYELKDAQHWMEKQVYLALGTL LLGAAALDVDACPMEGFDAKVLDDELGLRG 196

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTEV 217
 KG+TS+ +V +G+ DFN LPKSRL + T++
 Sbjct: 197 KGFTSVALVGLGYSGEEDFNKALPKSRLADEVVFTDI 233

☐ >gi|23104144|ref|ZP_00090612.1| COG0778: Nitroreductase [Azotobacter vinelandii]
 Length = 196

Score = 195 bits (496), Expect = 4e-49
 Identities = 96/188 (51%), Positives = 127/188 (67%)

Query: 28 EQIKTLLQYSPSSSTNSQPWHFIVASTEELGKARVAKSAAGNYVFNERKMLDASHVVVFCAK 87
 E+++TLL+YSPSS NSQPWH ++A+++EGKAR+AK+ Y +NE K+L+ASHVVV CA+
 Sbjct: 7 EELQTLLRYSPSSVNSQPWHHVIAASDEGKARIAKATQDGYAYNEAKILNASHVVVLCAR 66

Query: 88 TAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADMHRKDLHDDAEWMAKQVYLVN 147
 T +D LK V++QED DGR+A PE KA R + ++HR D D WM KQVYL +
 Sbjct: 67 TDLDAHLKAVLNQEDLDGRYANPEGKAGQGNVRSSVYNLHRYDRKDLQHWMEKQVYLAL 126

Query: 148 GNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLEKEKGYTSLVVVPVGHHSVEDFNATLPKSR 207
 G PIEGFD LD E GL+E+G+TS+V+V +G+ S +DFNA LPKSR
 Sbjct: 127 GTLLLGAAASGV DATPIEGFDFHRLDEELGLRERGETSVVIVSLGYRSEDDFNAKLPKSR 186

Query: 208 LPQNITLT 215
 LP T
 Sbjct: 187 LPTEDIPT 194

☐ >gi|22980342|ref|ZP_00026049.1| COG0778: Nitroreductase [Ralstonia metallidurans]
 Length = 220

Score = 182 bits (463), Expect = 3e-45
 Identities = 95/215 (44%), Positives = 136/215 (63%)

Query: 1 MDIISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEELGKARV 60
 M + + RH+ KA++ + + + +++ +L SPSS NSQPWHF+VAST E +ARV
 Sbjct: 4 MKLSEMIATRHTVKAYEPGRAIPQDVIDELLAVLHKSPSSVNSQPWHFVVASTPEARARV 63

Query: 61 AKSAAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKG 120
 A++A+G Y N ++ +ASHV+ + MD+ L +++ E+ DGRF AKA DKG
 Sbjct: 64 ARAASGGYSANAPRIENASHVIALAVRADMDNAHLNKLLEAEERDGRFTAEGAKAGQDKG 123

Query: 121 RKFFADMHRKDLHDDAEWMAKQVYLVN GNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLEKE 180
 R++F D+HR D +WMA QVYL +G+ P+EGFD ILDAE GL+E
 Sbjct: 124 RRYFVDLHRFAFRDVQQWMANQVYLALGSLTGA AVLGV DATPMEGFDRNILD AELGLRE 183

Query: 181 KGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLT 215
 +GYTSLV+V +G+ S +DFNA LPKSRL + T
 Sbjct: 184 RGYTSLVLVSLGYGSEQDFNADLPKSRLGKEEVFT 218

☐ >gi|23476096|ref|ZP_00131306.1| COG0778: Nitroreductase [Desulfovibrio desulfuri]
 Length = 124

Score = 108 bits (270), Expect = 7e-23
Identities = 51/100 (51%), Positives = 69/100 (69%)

Query: 4 ISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKS 63
I R++TK FD ++L E + +K +LQ SPSSTNSQPWHF++A T+EG+ RVAK+
Sbjct: 25 IEALTTRYTTKKFDPDRRLDAETVQAVKDILQLSPSSTNSQPWHFVIAGTDEGRQVAKA 84

Query: 64 AAGNYVFNERKMLDASHVVVFCAKTAMDDVWLKLVVDQED 103
A G Y FN K+ DASHVVV C KT +D + V++QE+
Sbjct: 85 AHGVYAFNASKICDASHVVVLCTKTDIDTEYTTQVLEQEE 124

>[gi|6016045|sp|P46072|FRA1_VIBFI](#) Major NAD(P)H-flavin oxidoreductase (FRASE I)
[gi|4558192|pdb|1VFR|A](#) Chain A, The Major Nad(P)h:fmn Oxidoreductase From Vibrio
[gi|4558193|pdb|1VFR|B](#) Chain B, The Major Nad(P)h:fmn Oxidoreductase From Vibrio
[gi|6539550|dbj|BAA04595.2](#) NAD(P)H-flavin oxidoreductase [Vibrio fischeri]
Length = 218

Score = 99.4 bits (246), Expect = 4e-20
Identities = 64/199 (32%), Positives = 100/199 (50%), Gaps = 3/199 (1%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNYV 69
R+++K +D SKK++ E + L+ S SS NSQPW FIV ++ K R+ S A +
Sbjct: 12 RYTSKKYDPSKKVSQEDLAVLLEALRLSASSINSQPWKFIVIESDAAKQRMHDSFANMHQ 71

Query: 70 FNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADMHR 129
FN+ + SHV++F K + +V+ + AD R + +AA + F +++
Sbjct: 72 FNQPHIKACSHVILFANKLSYTRDDYDVVLSKAVADKRITEEQKEAAFASF--FVELNC 129

Query: 130 KDLHDDAEWMAKQVYLVNMGNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKEKGYTSLVVV 189
+ + W Q YL +GN +EG D +L F + KGY V +
Sbjct: 130 DENGHEKAWTKPQAYLALGNALHTLARLNIDSTTMEGIDPELLSEIFADELKGYECHVAL 189

Query: 190 PVG-HHSVEDFNATLPKSR 207
+G HH ED+NA+LPKSR
Sbjct: 190 AIGYHHPSSEDYNASLPKSR 208

>[gi|28900963|ref|NP_800618.1](#) putative NAD(P)H-flavin reductase [Vibrio parahaer
2210633]
[gi|28809409|dbj|BAC62451.1](#) putative NAD(P)H-flavin reductase [Vibrio parahaemoly
Length = 244

Score = 94.0 bits (232), Expect = 2e-18
Identities = 60/207 (28%), Positives = 95/207 (45%), Gaps = 3/207 (1%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNYV 69
R++ K +DA K+++ E IK ++ S SS NSQPW FIV ++E K R + A +
Sbjct: 38 RYTAKKYDAEKRIQEDMAIIEAIRLSASSINSQPWKFIVIESDEAKQRFHSTFANKHQ 97

Query: 70 FNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADMHR 129
FN+ ASH ++ VD E G P G FA+ +
Sbjct: 98 FNQPHATTASHTILLAYDPKFTKEKFAKRVDAEVTSGHL--PADMYNTFMGAYAFAEANT 155

Query: 130 KDLHDDAEWMAKQVYLVNMGNFXXXXXXXXXXXXXPIEGFDAAILDAEFGLKEKGYTSLVVV 189
+ + W QVY+ +GN P+EG D ++ EF + +G+ V +

Sbjct: 156 DENGFNHWTAKQVYIALGNLLHTLARLGIDSTPMEGVDPELIGEEFKDELEGHVCEVAL 215

Query: 190 PVGHHS-VEDFNATLPKSRLPQNITLT 215

+G+H ED+N LPK+R+ + +T

Sbjct: 216 AIGYHKDGEDYNHGLPKARMALDDVIT 242

>gi|22299744|ref|NP_682991.1| nitroreductase [Thermosynechococcus elongatus BP-1]
gi|22295928|db|BAC09753.1| nitroreductase [Thermosynechococcus elongatus BP-1]
Length = 218

Score = 92.0 bits (227), Expect = 7e-18

Identities = 63/206 (30%), Positives = 97/206 (47%), Gaps = 19/206 (9%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEKGKARVAKSAAGNYV 69
R++TK FD ++K+ + + L +PSS QPW F V T E + A +

Sbjct: 18 RYATKKFDPNRKIPAHLWQTLQLSLVLAPSSFGLQPWKFYVIETPE-----LRQALLPHT 72

Query: 70 FNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADMHR 129
+N+R+++DASH+VVF K+ ++ D + R A + D R + D+ +

Sbjct: 73 WNQRQVVDASHLVVFAIKSHLN-----AADVDRLARQAEVRQTSMEDLQR--YGDLVK 124

Query: 130 KDLHDDA-----EWMKQVYLVNNGNFXXXXXXXXXXXXXXPIEGFDAAILDAEFGLEKEGY 183
LH EW A+QVY+ +G F P+EGF D L +GY

Sbjct: 125 GFLHSPPYPLNVDEWSARQVYIALGQFMVTAALLGIDTCPMEGFLPQEYDRLLDLPAQGY 184

Query: 184 TSLVVVPVGHHSVEDEFNATLPKSRLP 209

++VV G+ + +D ATLEK R P

Sbjct: 185 HAVVCAAGYRAADDQYATLPKVRYP 210

>gi|15890499|ref|NP_356171.1| AGR_L_768p [Agrobacterium tumefaciens]
gi|25519409|pir|B98179 probable NAD(P)H nitroreductase yfko [imported] - Agrobac
tumefaciens (strain C58, Cereon)
gi|15158735|gb|AAK88956.1| AGR_L_768p [Agrobacterium tumefaciens str. C58 (Cereon)
Length = 271

Score = 76.6 bits (187), Expect = 3e-13

Identities = 54/206 (26%), Positives = 100/206 (48%), Gaps = 19/206 (9%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEKGKARVAKSAAGNYV 69
R++TK D SK + ++ E+I + +P+S+ QP+ IV + E +A++ + A

Sbjct: 71 RYATKKMDPSKTVAEDKVERIVEAARLAPTSSGLQPFEVIVVTDPEVRAKIREIA----- 125

Query: 70 FNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADM-- 127
+N+ ++ + SH++VF A + + + D + E + ++G + + M

Sbjct: 126 WNQAQVTEGSHLLVFAAWDNYTEERINHMFDLVN-----EERGIKNEGWEAYRQMLL 177

Query: 128 ---HRKDLHDDAEWMKQVYLVNNGNFXXXXXXXXXXXXXXPIEGFDAAILDAEFGLEKEGYT 184
++D + E A+Q Y+ G P+EGF A LD GL+EKG

Sbjct: 178 TTYPQRDQQVNFEHAARQAYIGFGMAVAQAFAEGVDSTPMEGFDPKLEILGLREKGLR 237

Query: 185 SLVVVPVGHHSVE-DFNATLPKSRLP 209

S+ ++P+G+ + D+ L K R P

Sbjct: 238 SVTILPLGYRQPDGDWLVNLKKVRRP 263

gi|17938175|ref|NP_534964.1| nitroreductase [Agrobacterium tumefaciens str. C58] gi|25523870|pir|AB3108 nitroreductase [imported] - Agrobacterium tumefaciens (s Dupont) gi|17742967|gb|AAL45280.1| nitroreductase [Agrobacterium tumefaciens str. C58 (U. Length = 209

Score = 75.1 bits (183), Expect = 8e-13

Identities = 54/206 (26%), Positives = 100/206 (48%), Gaps = 19/206 (9%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEKGKARVAKSAAGNYV 69
R++TK D SK + ++ E+I + +P+S+ QP+ IV + E +A++ + A
Sbjct: 9 RYATKKMDPSKTVAEDKVERIVEAARLAPTSSGLQPFEVIVVTDPEVRAKIREIA----- 63

Query: 70 FNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADM-- 127
+N+ ++ + SH++VF A + + + D + E + ++G + + M
Sbjct: 64 WNQAQVTEGSHLLVFAAWDNYTEERINHMFDLVN-----EERGIKNEGWEAYRQMLL 115

Query: 128 ---HRKDLHDDAEWMAKQVYLVGNFXXXXXXXXXXXXXPIEGFDAAILDAEFLKEKGYT 184
++D + E A+Q Y+ G P+EGFD A LD GL+EKG
Sbjct: 116 TTYPQRDQQVNFEEHAARQAYIGFGMAVAQAAFEGVDSTPMEGFDPKALDEILGLREKGLR 175

Query: 185 SLVVVPVGHHSVE-DFNATLPKSRLP 209
S+ ++P+G+ + D+ L K R P
Sbjct: 176 SVTILPLGYRQPDGDWLVNLKKVRRP 201

gi|16125698|ref|NP_420262.1| nitroreductase family protein [Caulobacter crescentus] gi|25397805|pir|B87429 nitroreductase family protein [imported] - Caulobacter crescentus gi|13422816|gb|AAK23430.1| nitroreductase family protein [Caulobacter crescentus] Length = 210

Score = 73.9 bits (180), Expect = 2e-12

Identities = 54/209 (25%), Positives = 99/209 (47%), Gaps = 9/209 (4%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEKGKARVAKSAAGNYV 69
R++ K D +K ++ ++ E+I + +P+S+ QP+ IV + E + ++ A G
Sbjct: 9 RYAAKKMDPAKVVEDKVERIVEAARLAPTSSGLQPFEIIVVTNAEVREKI--KAIG--- 63

Query: 70 FNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADMHR 129
+N+ + D SH++VF A D+ + + D + + + + +
Sbjct: 64 WNQSPITDGSHELLVF---AAWDNYTAERINHMFDLVNEVRGFRNEGWENYRQMLLSAYPQ 120

Query: 130 KDLHDDAEWMAKQVYLVGNFXXXXXXXXXXXXXPIEGFDAAILDAEFLKEKGYTSLVVV 189
+D + E A+Q Y+ G P+EGFD LD GL+E+G S+ +
Sbjct: 121 RDPETNFEHAARQAYIAFGLALAAQAFAEGVDATPMEGFDPKALDEILGLRERGLRSVTIA 180

Query: 190 PVGHHSVE-DFNATLPKSRLPQNITLTEV 217
P+G+ VE D+ L K R P++ +TEV
Sbjct: 181 PLGYRQVEGDWLVNLQKVRPRDQFVTEV 209

gi|32030652|ref|ZP_00133458.1| COG0778: Nitroreductase [Haemophilus somnus 2336] Length = 220

Score = 68.6 bits (166), Expect = 8e-11


Identities = 65/225 (28%), Positives = 102/225 (45%), Gaps = 36/225 (16%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +R ST+ +D +KK++ E + + SPSS S+PWHF+V E +A++ + G
 Sbjct: 15 RRASTRYYDPNKKISDEDFSYVLEFARLSPSSVGSEFPWHFLVIQNPELRAKLKPVSWGMA 74

Query: 69 VFNERKMLDASHVVVFCAC--TAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFAD 126
 ++ DASH+VV AK D +L + + G + +A +K F A+
 Sbjct: 75 T----QIDDASHLVVILAKKNARYDSEFLVQSMKRRGLSGE----QIQATKEKYHLFQAE 126

Query: 127 MHRKDLHDDA---EWMKQVYVLNVGNFXXXXXXXXXXXXPIEGF-----DAAILD 173
 H K L +D +W +KQ Y+ + N PIEGF DA +LD
 Sbjct: 127 -HMKTLENDRTLFDWASKQTYIALANMLTGAALIGIDSCPIEGFNYEKNQILTDAGVLD 185

Query: 174 A-EFGLKEKGYTSLVVVPVGHHSVEDFNATLPKSRLPQNITLTV 217
 + E+G+ V+ G+ + E PKSR N +T V
 Sbjct: 186 SDEWGV-----VMATFGYRAKE----IKPKSRKSLNEIVTWV 219

 >gi|23466763|ref|ZP_00122352.1| COG0778: Nitroreductase [Haemophilus somnus 129]
 Length = 220


Score = 68.6 bits (166), Expect = 8e-11
 Identities = 59/209 (28%), Positives = 97/209 (46%), Gaps = 28/209 (13%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +R ST+ +D +KK++ E + + SPSS S+PWHF+V E +A++ + G
 Sbjct: 15 RRASTRYYDPNKKISNEDEFSYVLEFARLSPSSVGSEFPWHFLVIQNPELRAKLKPVSWGMA 74

Query: 69 VFNERKMLDASHVVVFCAC--TAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFAD 126
 ++ DASH+VV AK D +L + + G + +A +K F A+
 Sbjct: 75 T----QIDDASHLVVILAKKNARYDSEFLVQSMKRRGLSGE----QIQATKEKYHLFQAE 126

Query: 127 MHRKDLHDDA---EWMKQVYVLNVGNFXXXXXXXXXXXXPIEGF-----DAAILD 173
 H K L +D +W +KQ Y+ + N PIEGF DA +LD
 Sbjct: 127 -HMKTLENDRTLFDWASKQTYIALANMLTGAALIGIDSCPIEGFNYEKNQILTDAGVLD 185

Query: 174 A-EFG---LKEKGYTSLVVVPVGHHSVED 198
 + E+G + GY + + P S+++
 Sbjct: 186 SDEWGVSVMATFGYRAKEIKPKSRKSLDE 214

 >gi|32033912|ref|ZP_00134183.1| COG0778: Nitroreductase [Actinobacillus pleuropneumoniae str. 4074]
 Length = 220

Score = 67.0 bits (162), Expect = 2e-10
 Identities = 61/212 (28%), Positives = 91/212 (42%), Gaps = 28/212 (13%)


Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNYV 69
 R +T+ +DASKK++ E I L + SPSS S+PW F+V +E + ++ A G
 Sbjct: 16 RRATRNYDASKKISDEDFAYILELARLSPSSVGSEFPWKFFVVIQNQELRNKLPVWAGMAA 75

Query: 70 FNERKMLDASHVVVFCAC--TAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFADM 127
 +M ASH+VV AK + D + K ++Q R T E +K +
 Sbjct: 76 ----QMDAASHLVVLLAKKNASHDSEYFKKALEQ----RGLTAEEM---EKTALYKQF 123

Query: 128 HRKDLHDDA-----EWMKQVYVLNVGNFXXXXXXXXXXXXPIEGFD----AAILD AEF 177

H +D+ +W +KQ Y+ +GN PIEGF+ IL
 Sbjct: 124 HVEDIKIAGNERALFDWCSKQTYIALGNMMSGAMIGIDSCPIEGFNVDANKILAEAGA 183

Query: 178 LKEKGYTSLVVVPVGHHSVEDFNATLPKSRLP 209
 Y V+ G+ + E PKSR P
 Sbjct: 184 FDPNEYGVSMATFGYRAGE-----IAPKSRKP 211

 >[gi|27468991|ref|NP_765628.1|](#) NAD(P)H-flavin oxidoreductase [Staphylococcus epic
 12228]
[gi|27316549|gb|AA005715.1|](#) NAD(P)H-flavin oxidoreductase [Staphylococcus epidermi
 12228]
 Length = 220


Score = 64.3 bits (155), Expect = 2e-09
 Identities = 56/196 (28%), Positives = 86/196 (43%), Gaps = 16/196 (8%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEKGKARVAKSAAGNYV 69
 RH+TK FD +KK++ E I + SPSS +PWHF+V +E + ++ Y
 Sbjct: 15 RHATKEFDPTKKISDEDFNTILETGRSLSPSSLGLEPWHFVVQNKELREKLKA-----YS 69

Query: 70 FNERKMLD-ASHVVVFCAK---TAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFA 125
 + +K LD ASH V+ A+ TA D L+ + + +D F
 Sbjct: 70 WGAQKQLDTASHFVLIFARKNVTADTDYVQHLLRGVKKYEEESTIPAFENKFDDFQESFHI 129

Query: 126 DMHRKDLHDDAEWMAKQVYLVNNGFNXXXXXXXXXXXXPIEGFD----AAILDAEFGLKEK 181
 + + L+D W +KQ Y+ + N PIEGFD IL E L +
 Sbjct: 130 ADNERTLYD---WASKQTYIALANMMTSAALLGIDSCPIEGFDLDKVTETLSDEGVLDTE 186

Query: 182 GYTSLVVVPVGHHSVE 197
 + V+V G+ + E
 Sbjct: 187 QFGISVMVGFYRAQE 202

 >[gi|15793971|ref|NP_283793.1|](#) putative NAD(P)H-flavin oxidoreductase [Neisseria
 Z2491]
[gi|11254584|pir|E81949](#) probable NAD(P)H-flavin oxidoreductase NMA1015 [imported]
 Neisseria meningitidis (strain Z2491 serogroup A)
[gi|7379717|emb|CAB84284.1|](#) putative NAD(P)H-flavin oxidoreductase [Neisseria meni
 Z2491]
 Length = 221

Score = 63.2 bits (152), Expect = 3e-09
 Identities = 57/186 (30%), Positives = 84/186 (45%), Gaps = 19/186 (10%)

Query: 3 IISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEKGKARVAK 62
 ++S R S + +DA++K++ E + I L + SPSS S+PW F+V E +
 Sbjct: 9 VLSAFKNRKRSCRHYDAARKISAEDFQFILELGRSLSPSSVGSEPWQFVVVQNPE-----IR 63

Query: 63 SAAGNYVFNERKMLD-ASHVVVFCA-KTAMDDVWLKLVVDQEDADGRFAT-PEAKAANDK 119
 A + + LD ASH+VVF A K A D L E R T P+A A +
 Sbjct: 64 QAIKPFWSGMADALDTASHLVVFLAKKNARFDSPFML----ESLKRRGVTEPDAMAKSLA 119

Query: 120 GRKFFADMHRKDLHDDA---EWMKQVYLVNNGFNXXXXXXXXXXXXPIEGFDAA----IL 172
 + F K L D +W +Q Y+ +GN P+EGF+ A +L
 Sbjct: 120 RYQAFQADDIKILDDSRALFDWCCRQTYIALGNMGTGAAMAGIDSCPVEGFNYADMERV 179

Query: 173 DAEFGL 178
 +FGL
 Sbjct: 180 SGQFGL 185

>gi|15676702|ref|NP_273846.1| NAD(P)H nitroreductase, putative [Neisseria meningitidis (strain MC58 serogroup B)]
gi|11254586|pir|C81155 NAD(P)H nitroreductase, probable NMB0804 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
gi|7226038|gb|AAF41217.1| NAD(P)H nitroreductase, putative [Neisseria meningitidis]
 Length = 221

Score = 62.8 bits (151), Expect = 4e-09
 Identities = 58/186 (31%), Positives = 83/186 (44%), Gaps = 19/186 (10%)

Query: 3 IISVALKRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEEGKARVAK 62
 ++S R S + +DA++K++ E + I L + SPSS S+PW FIV E +
 Sbjct: 9 VLSAFKNRKRSCRHYDAARKISAEDFQFILELGRISPSSVGSEPWQFIVVQNPE-----IR 63

Query: 63 SAAGNYVFNERKMLD-ASHVVVFCA-KTAMDDVWLKLVVDQEDADGRFAT-PEAKAANDK 119
 A + + LD ASH+VVF A K A D L E R T P+A A +
 Sbjct: 64 QAIKPFWSGMADALDTASHLVVFLAKKNARSDSPFML----ESLKRRGVTEPDAVAKSLA 119

Query: 120 GRKFFADMHRKDLHDDA---EWMKQVYLVNNGFXXXXXXXXXXXXPIEGFDAA----IL 172
 + F K L D +W +Q Y+ + N P+EGF+ A IL
 Sbjct: 120 RYQAFQADDIKILDDSRALFDWCCRQTYIALANMMTGAAMAGIDSCPVEGFNYAEMERIL 179

Query: 173 DAEFGL 178
 +FGL
 Sbjct: 180 SGQFGL 185

>gi|9858504|gb|AAG01064.1| RdxA [Helicobacter pylori]
 Length = 210

Score = 62.4 bits (150), Expect = 5e-09
 Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +RHS K FD+ + + + E+I + + SPSS N+QPWHF++ + ++ K ++ AA +Y
 Sbjct: 15 ERHSCKMFDSHYEFSSTELEEIAEIAIRLSPSSSYNTQPWHFVIVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFCA 86
 FNE + AS ++V C+
 Sbjct: 72 -FNEEMIKSASALIVVCS 88

>gi|34558820|gb|AAQ75164.1| NAD(P)H-flavin oxidoreductase [Alvinella pompejana]
 Length = 207


Score = 62.0 bits (149), Expect = 7e-09
 Identities = 50/195 (25%), Positives = 90/195 (46%), Gaps = 10/195 (5%)

Query: 1 MDIISVALK-RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEEGKAR 59
 MD S L RH+ K FD +KK++ + ++I + SPSS + W F+V + +E KA+
 Sbjct: 1 MDSFSDILNFRHACKEFDETKKISDKDIKEILEAGRLSPSSFGMEGWKFLVTTNQLKAK 60

Query: 60 VAKSAAGNYVFNERKMLDASHVVVFCAMDDVWLKLVVDQEDADGRFATPEA-KAAND 118
 + +N++++ SH+V++ TA++ + K V + + E KA +
 Sbjct: 61 IRP-----LCWNQKQITSCSHLVIYL--TAIESLLPKSGVPAKRLSRKGIDEEMLKAYIE 113

Query: 119 KGRKFFADMHRKDLHDDAEWMAKQVYLVGNFXXXXXXXXXXXXPIEGFDAAILDAEFG 178
 K F D + W AKQ Y+ + + PIEGF+ L+ +
 Sbjct: 114 KYSNFLEDKLNSS-NGIYHWGAKQTYIAMTSMMLASASLGVDSCPIEGFEKEPLEKLLNI 172


Query: 179 KEKGYTSLVVVPVGH 193
 Y +++P+G+
 Sbjct: 173 DTSKYQITLLLPLGY 187

 >gi|9858534|gb|AAG01077.1| RdxA [Helicobacter pylori]
 Length = 210

Score = 62.0 bits (149), Expect = 7e-09
 Identities = 28/78 (35%), Positives = 47/78 (60%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +RHS K FD+ + + E+I + + SPSS N+QPWHF++ + ++ V K A +
 Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAEIARLSPSSYNTQPWHFVMVTNKD----VKKQIAAHS 70


Query: 69 VFNERKMLDASHVVVFC 86
 FNE + AS ++V C+
 Sbjct: 71 YFNEEMIKSASALMVVCS 88

 >gi|17225177|gb|AAL37285.1| oxygen-insensitive NADPH nitroreductase [Helicobacter pylori]
 Length = 210

Score = 62.0 bits (149), Expect = 8e-09
 Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +RHS K FD+ + + E+I + + SPSS N+QPWHF++ + ++ K ++ AA +Y
 Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAEIARLSPSSYNTQPWHFVIVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFC 86
 FNE + AS ++V C+
 Sbjct: 72 -FNEEMIKSASALMVVCS 88

 >gi|9858502|gb|AAG01063.1| RdxA [Helicobacter pylori]
 Length = 210

Score = 61.6 bits (148), Expect = 8e-09
 Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +RHS K FD+ + + E+I + + SPSS N+QPWHF++ + ++ K ++ AA +Y
 Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAEIARLSPSSYNTQPWHFVIVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFC 86
 FNE + AS ++V C+
 Sbjct: 72 -FNEEMIKSASALMVVCS 88

gi|17225185|gb|AAL37289.1| oxygen-insensitive NADPH nitroreductase [Helicobacter pylori]
Length = 210

Score = 61.6 bits (148), Expect = 9e-09
Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEELGKARVAKSAAGNY 68
+RHS K FD+ + + + E+I + + SPSS N+QPWHF++ + ++ K ++ AA +Y
Sbjct: 15 ERHSCKMFDShyEFSSTELEEIAEIRLSPSSSYNTQPWHFVIVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFCA 86
FNE + AS ++V C+
Sbjct: 72 -FNEEMIKSASALMVVCS 88

gi|23100581|ref|NP_694048.1| NAD(P)H nitroreductase [Oceanobacillus iheyensis]
gi|22778814|dbj|EAC15082.1| NAD(P)H nitroreductase [Oceanobacillus iheyensis HTE8]
Length = 222

Score = 61.6 bits (148), Expect = 9e-09
Identities = 57/208 (27%), Positives = 94/208 (45%), Gaps = 23/208 (11%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEELGKARVAKSAAGNYV 69
RH+TK +D SKK+ E + I + SPSS +PW F++ + + + ++ + A+G
Sbjct: 18 RHATKEYDGSKKIEDDFKFILETGRLSPSSSLGLEPWKFLIVQSSDLREKLMQLASG--- 74

Query: 70 FNERKMLDASHVVVFCAKTAM---DDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFA 125
ER++ ASH V+ A+ + D V L Q+ D E KG K F
Sbjct: 75 -AERQLSGASHFVIILARVDVRYDSYVANHLRTVQQMPD-----EVADMLLKGIKTFQ 127

Query: 126 DMHRKDLHDDA--EWMKQVYLVNMGVXXXXXXXXXXXXPIEGFDAA----ILDAEFGLK 179
+ + +D +W +KQ Y+ + N PIEGF +L++E L+
Sbjct: 128 ENFLQLFNDRTLFWDSSKQTYIALANMMTAAQAIGIDSTPIEGFIYKDVHNLLESEGLLE 187

Query: 180 EKGYSLSLVVVPVGHHSVEDFNATLPKSR 207
+ Y V+ G+ E + PK+R
Sbjct: 188 DGRYQPSVMAAFGYRKEE---PSRPKTR 212

gi|16077850|ref|NP_388664.1| similar to NAD(P)H-flavin oxidoreductase [Bacillus subtilis]
gi|3915460|sp|O34475|YFKO_BACSU Putative NAD(P)H nitroreductase yfkO
gi|7432647|pir|B69809 NAD(P)H-flavin oxidoreductase homolog yfkO - Bacillus subtilis
gi|2626827|dbj|BAA23405.1| YfkO [Bacillus subtilis]
gi|2633107|emb|CAB12612.1| yfkO [Bacillus subtilis subsp. subtilis str. 168]
Length = 221

Score = 61.6 bits (148), Expect = 1e-08
Identities = 59/211 (27%), Positives = 91/211 (43%), Gaps = 27/211 (12%)

Query: 10 RHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEELGKARVAKSAAGNYV 69
RH+TK FD +KK++ E I + SPSS +PW F+V E + ++ + G
Sbjct: 15 RHATKEFDPNKKVSDSDFEFILETGRLSPSSSLGLEPWKFVVVQNPEFREKLREYTWG--- 71

Query: 70 FNERKMLDASHVVVFCAKTAMDDVWLKLVVDQEDADGRFATPEAKAANDKGRKFFA---D 126



```

      +++++ ASH V+  A+TA D      +   D   R      +   D   + +   +
Sbjct: 72  -AQKQLPTASHFVLILARTAKD-----IKYNADYIKRHLKEVKQMPQDVYEGYLSKTEE 124

Query: 127 MHRKDLH-----DDA--EWMKQVYLVNNGNXXXXXXXXXXXXXPIEGFD-----AAILDAEF 176
      + DLH      D      +W +KQ Y+ +GN                      PIEGF      IL+ E
Sbjct: 125 FQKNDLHLLSDRTLFDWASKQTYIALGNMMTAAQIGVDSCPIEGFQYDHIHRILEEE- 183

Query: 177 GLKEKGYTSLVVVPVGHHSVEDFNATLPKSR 207
      GL E G      + V+      + V D      PK+R
Sbjct: 184 GLENGSFDISVMVAFGYRVRD---PRPKTR 211

```

 >[gi|9858494|gb|AAG01059.1|](#) RdxA [Helicobacter pylori]
Length = 210


Score = 61.2 bits (147), Expect = 1e-08
Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

```

Query: 9  KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEKGKARVAKSAAGNY 68
      +RHS K FD+  + +  + E+I  + + SPSS N+QPWHF++ + ++ K ++  AA +Y
Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAEIA RLSPSSYNTQPWHFVMVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFCA 86
      FNE  +  AS ++V C+
Sbjct: 72 -FNEEMIKSASALMVVCS 88

```

 >[gi|2564445|gb|AAC46351.1|](#) NADPH-linked flavin nitroreductase [Helicobacter pylori]
Length = 196


Score = 61.2 bits (147), Expect = 1e-08
Identities = 27/78 (34%), Positives = 48/78 (61%), Gaps = 4/78 (5%)

```

Query: 9  KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEKGKARVAKSAAGNY 68
      +RHS K FD+  + +  + E+I  + + SPSS N+QPWHF++ + ++ K ++A  +
Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAEIA RLSPSSYNTQPWHFVMVTNKDVKNQIATHS---- 70

Query: 69 VFNERKMLDASHVVVFCA 86
      FNE  +  AS ++V C+
Sbjct: 71 YFNEEMIKSASALMVVCS 88

```

 >[gi|17225181|gb|AAL37287.1|](#) oxygen-insensitive NADPH nitroreductase [Helicobacter pylori]
Length = 210

Score = 61.2 bits (147), Expect = 1e-08
Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

```

Query: 9  KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEKGKARVAKSAAGNY 68
      +RHS K FD+  + +  + E+I  + + SPSS N+QPWHF++ + ++ K ++  AA +Y
Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAEIA RLSPSSYNTQPWHFVMVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFCA 86
      FNE  +  AS ++V C+
Sbjct: 72 -FNEEMIKSASALMVVCS 88

```

>gi|9858514|gb|AAG01069.1| RdxA [Helicobacter pylori]
gi|17225169|gb|AAL37281.1| oxygen-insensitive NADPH nitroreductase [Helicobacter]
gi|17225171|gb|AAL37282.1| oxygen-insensitive NADPH nitroreductase [Helicobacter]
 Length = 210

Score = 61.2 bits (147), Expect = 1e-08
 Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +RHS K FD+ + + + E+I + + SPSS N+QPWHF++ + ++ K ++ AA +Y
 Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAE IARLSPSSYNTQPWHFVMVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFCA 86
 FNE + AS ++V C+
 Sbjct: 72 -FNEEMIKSASALMVVCS 88

>gi|9858492|gb|AAG01058.1| RdxA [Helicobacter pylori]
 Length = 210

Score = 61.2 bits (147), Expect = 1e-08
 Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +RHS K FD+ + + + E+I + + SPSS N+QPWHF++ + ++ K ++ AA +Y
 Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAE IARLSPSSYNTQPWHFVMVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFCA 86
 FNE + AS ++V C+
 Sbjct: 72 -FNEEMIKSASALMVVCS 88

>gi|19774226|gb|AAL55409.1| NADPH nitroreductase RdxA [Helicobacter pylori]
gi|19774229|gb|AAL55408.1| NADPH nitroreductase RdxA [Helicobacter pylori]
 Length = 209

Score = 60.8 bits (146), Expect = 1e-08
 Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSTNSQPWHFIVASTEEGKARVAKSAAGNY 68
 +RHS K FD+ + + + E+I + + SPSS N+QPWHF++ + ++ K ++ AA +Y
 Sbjct: 15 ERHSCKMFD SHYEFSSTELEEIAE IARLSPSSYNTQPWHFVMVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFCA 86
 FNE + AS ++V C+
 Sbjct: 72 -FNEEMIKSASALMVVCS 88

>gi|9858531|gb|AAG01076.1| RdxA [Helicobacter pylori]
 Length = 210

Score = 60.8 bits (146), Expect = 1e-08
 Identities = 29/78 (37%), Positives = 50/78 (64%), Gaps = 4/78 (5%)

Query: 9 KRHSTKAFDASKKLTPEQAEQIKTLLQYSPSSSTNSQPWHFIVASTEKGARVAKSAAGNY 68
 +RHS K FD+ + + + E+I + + SPSS N+QPWHF++ + ++ K ++ AA +Y
 Sbjct: 15 ERHSCKMFDShyEFSSTELEEIAEIAIRLSPSSYNTQPWHFVMVTNKDLKKQI---AAHSY 71

Query: 69 VFNERKMLDASHVVVFCA 86
 FNE + AS ++V C+
 Sbjct: 72 -FNEEMIKSASALMVVCS 88

Database: All non-redundant GenBank CDS
 translations+PDB+SwissProt+PIR+PRF
 Posted date: Dec 29, 2003 2:09 AM
 Number of letters in database: 519,349,222
 Number of sequences in database: 1,585,607

Lambda	K	H
0.316	0.131	0.378

Gapped

Lambda	K	H
0.267	0.0410	0.140

Matrix: BLOSUM62
 Gap Penalties: Existence: 11, Extension: 1
 Number of Hits to DB: 20,015,580
 Number of Sequences: 1585607
 Number of extensions: 713568
 Number of successful extensions: 1607
 Number of sequences better than 10.0: 22
 Number of HSP's better than 10.0 without gapping: 16
 Number of HSP's successfully gapped in prelim test: 6
 Number of HSP's that attempted gapping in prelim test: 1582
 Number of HSP's gapped (non-prelim): 23
 length of query: 217
 length of database: 519,349,222
 effective HSP length: 119
 effective length of query: 98
 effective length of database: 330,661,989
 effective search space: 32404874922
 effective search space used: 32404874922
 T: 11
 A: 40
 X1: 16 (7.3 bits)
 X2: 38 (14.6 bits)
 X3: 64 (24.7 bits)
 S1: 41 (21.7 bits)
 S2: 71 (32.0 bits)